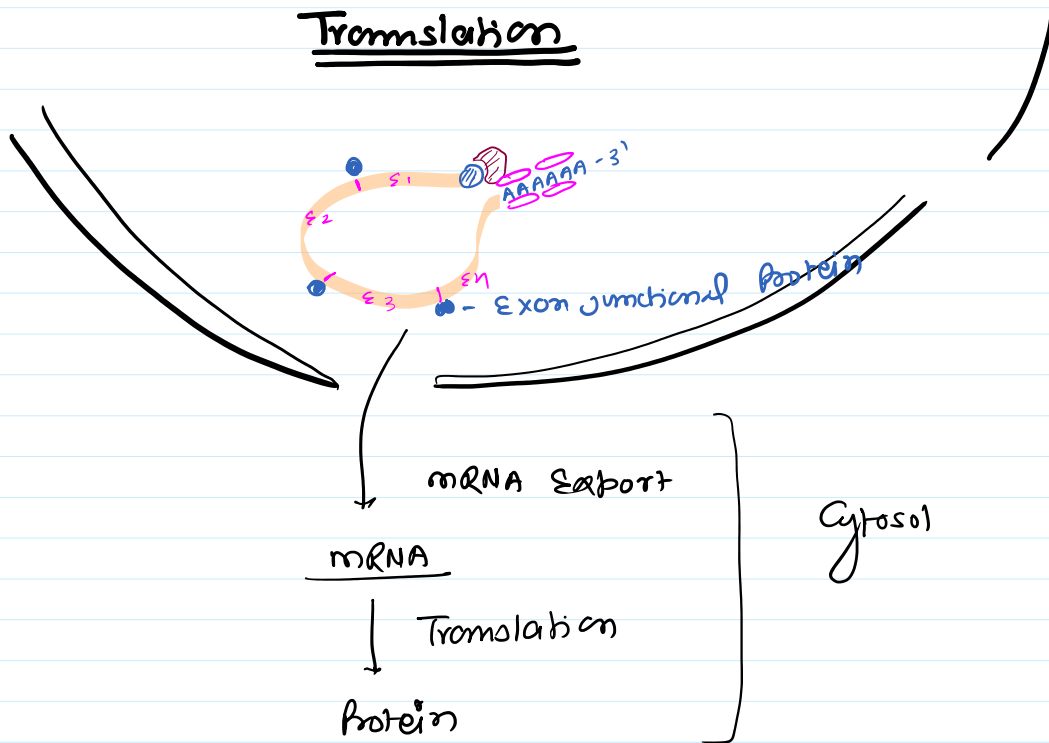


Translation

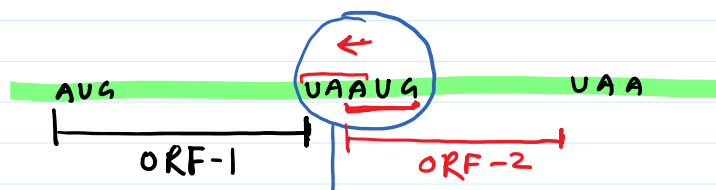


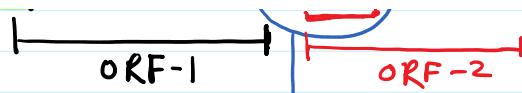
Translation

- mRNA
 - tRNA
 - Ribosome
- Basic Requirement for Translation

* Prokaryotic Translation

- Coupled Translation [with Transcription]
 - mRNA Contain Ribosomal Binding site
 - ↓
 - K/a Shine Dalgarno Seq.
- in prokaryotic mRNA, multiple open Reading frame is +nt
- ↓
 - K/a Polycistronic mRNA

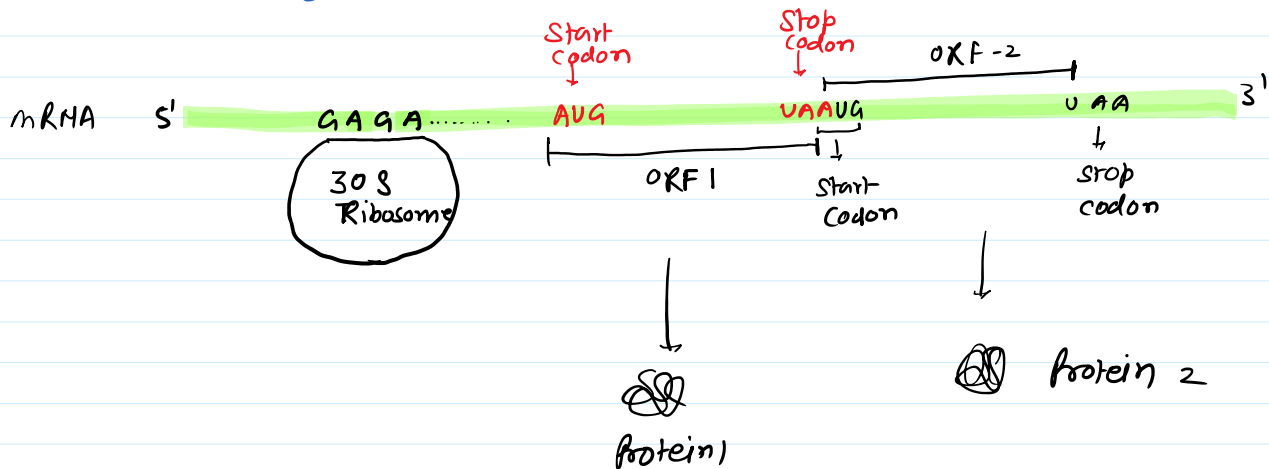




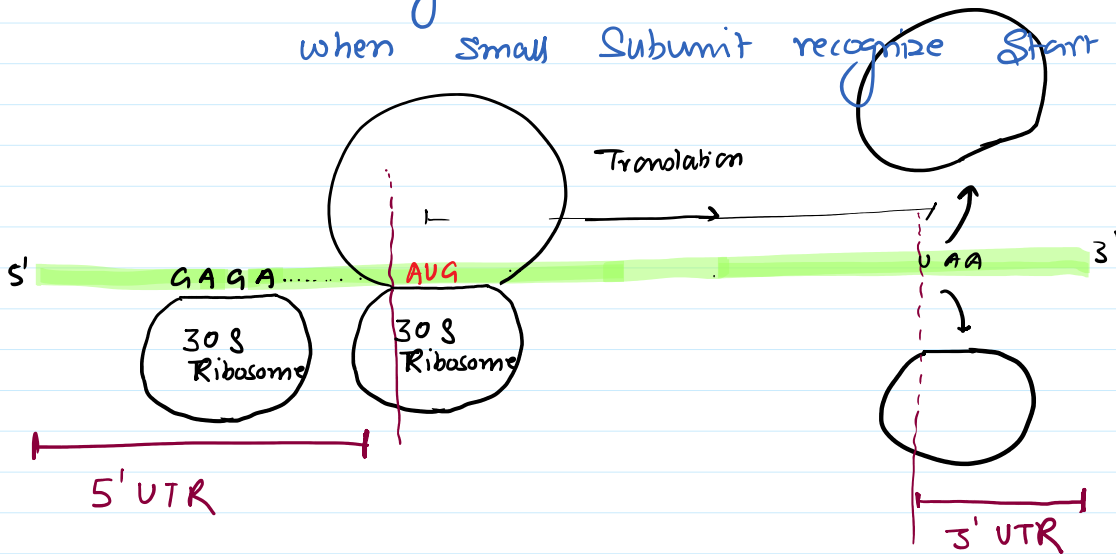
Translation coupling for Translation of ORF-2

◦ 70S Type Ribosome is required for Translation

- Small Subunit = 30S → recognize RBS [S.D. seq.] on mRNA
- Large subunit = 50S = catalytic activity



* Large Subunit has affinity for Small Subunit but large Subunit is associated with Small Subunit when Small Subunit recognize Start codon



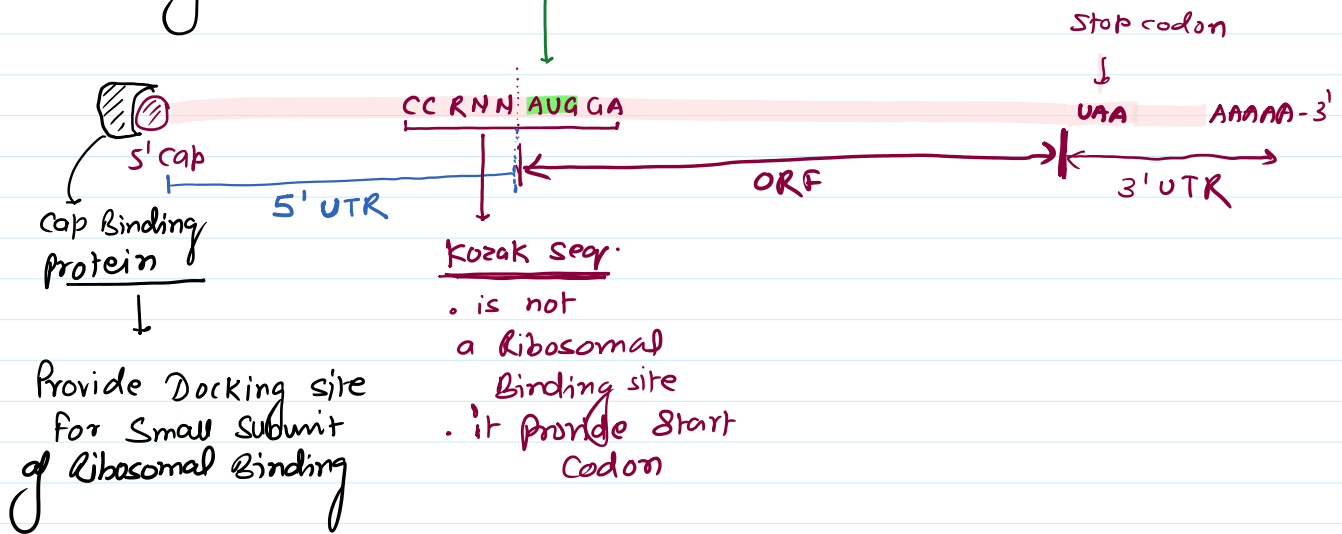
Eukaryotic mRNA

Start codon

R = Purine
N = any Nt.

Stop codon

Eukaryotic mRNA



Eukaryotic Translation

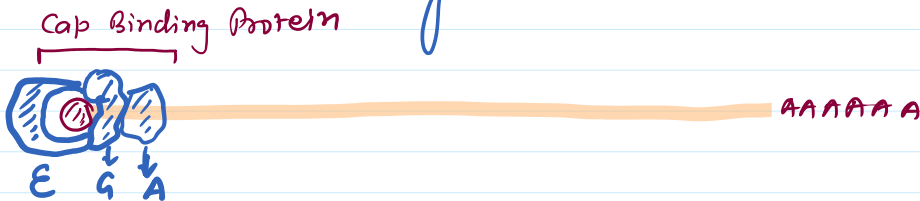
- Single ORF +nt in mRNA [monocistronic mRNA]
- Exception = 18S rRNA, 5.8S rRNA, 28S rRNA (Polycistronic)

- 80S type Ribosome involved in Translation

- 5' UTR → Contain Kozak Seq.

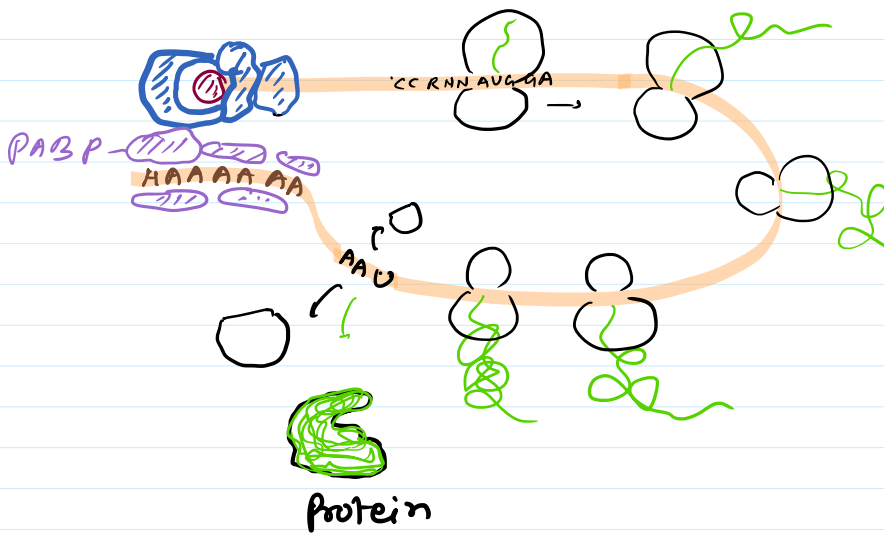
↓
Contain Translation Start Site
(Start codon)

- Cap Binding Protein act as Docking site for Small subunit of Ribosome



EIF - 4E
EIF - 4G
EIF - 4A

Binding site for
Small subunit of Ribosome



mRNA Contain Genetic code → Kila Codon

→ AUC - CAG - GUA - CAC -
 a_1 a_2 a_3 a_n
 1 codon

Codon

① Triplet

- 3nt. Codes for 1 a.a.
- total No. of Bases = 4 [AUCG = in mRNA]
- Total No. of Standard a.a. = 20

if Codon were single = $4^1 = 4$ codon
 Base

if codon were duplet = $4^2 = 16$ codon

Codon is Triplet = $4^3 = 64$ codon

Codon = 64

Stop codon = 3

leads to

61 codons are codes for

Leads to
Codon Redundancy
or
Codon degeneracy

codon = 3

61 codons are codes for
20 different a.a.

② Codon Redundancy / Codon degeneracy ⇒

- Single a.a. can be coded by more than 1 type of codon but every codon codes for only 1 a.a.

eg. 6 codon + nt for = L, S, R

4 codon = P, T, G, A

Que → On Mars → organism DNA

↓
3 base [A, U, C]

→ Protein = 50 types of a.a.

Codon = ?

$$3 \times 3 \times 3 = 27$$

X if codon triplet = $3^3 = 27$ codon

codon is Tetraplet = $3^4 = 81$ Codon

$$3 \times 3 \times 3 \times 3 = 81$$

③ Codon is Universal

- meaning of codon is almost same in different organism

eg: UUU → codes for Phenyl ala. in all 3 domain of life

Exceptions

codon

General

Yeast & mammalian

Exceptions

Codon	General meaning	<u>Yeast & mammalian</u> <u>mt</u>
<u>AGG</u>	[<u>Arg</u>]	Stop
<u>AGA</u>		
<u>UGA</u>	Stop	Trp

Exception in Bacteria-

$\left. \begin{matrix} \text{AUG} \\ \text{GUG} \\ \text{CUG} \end{matrix} \right\}$ all 3 codon may act as start codon

AUG* \rightarrow most common start codon
 Code's for formyl methionine

④ Codon Bias

eg. ① Proline $\rightarrow \left[\begin{matrix} \text{CCU} \\ \text{CCC} \\ \text{CCA} \end{matrix} \right]$ - less preferred
 $\rightarrow \text{CCG}$ \rightarrow most preferred codon

② UAA \rightarrow is most preferred stop codon

$\left[\begin{matrix} \text{UGA} \\ \text{UAG} \end{matrix} \right]$ - less preferred stop codon

Codon Bias \rightarrow Codons are equal in meaning
 But not equal in function

⑤ Codons are commas less and non-overlapping

5' \rightarrow AUG CCA GAC UAC GAC UUU UAA \rightarrow 3'
 $\downarrow \quad \downarrow \quad \downarrow \quad \downarrow \quad \downarrow \quad \downarrow \quad \downarrow$
 $- a_1 - a_2 - a_3 - a_4 - a_5 - a_6 - X = \text{No. of a.a. } 6$

$a_1 - a_2 - a_3 - a_n - a_3 - a_5 - X$ = No. of a.a. 6
 Type of a.a. 5

U	C	A	G
UUU } Phe UUC } UUA } Leu UUG }	^{1 2 3} UCU } UCC } Ser UCA } UCG }	UAU } Tyr UAC } UAA } Stop UAG } Stop	UGU } Cys UGC } UGA } Stop UGG } Trp
CUU } CUC } Leu CUA } CUG }	CCU } CCC } Pro CCA } CCG }	CAU } His CAC } CAA } Gln CAG }	CGU } CGC } Arg CGA } CGG }
AUU } Ile AUC } AUA } AUG } Met	ACU } ACC } Thr ACA } ACG }	AAU } Asn AAC } AAA } Lys AAG }	AGU } Ser AGC } AGA } Arg AGG }
GUU } GUC } Val GUA } GUG }	GCU } GCC } Ala GCA } GCG }	GAU } Asp GAC } GAA } Glu GAG }	GGU } GGC } Gly GGA } GGG }
Non-polar a.a.		Polar a.a.	

Stop codon: UAA → ochre → most preferred stop codon
 UAG → amber
 UGA → opal

In codon maximum degeneracy provided by
 3rd position of codon

eg - ala - codon

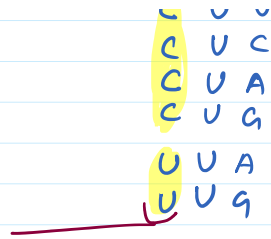
1 2 3
 G C U
 G C C
 G C A
 G C G

→ codes for ala.

↳ max. degeneracy position

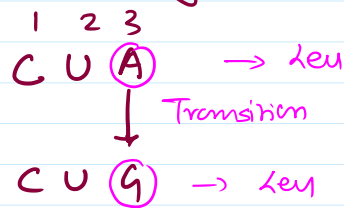
Degeneracy also can be seen in 1st position of codon
 eg. leucine

1 2 3
 C U U
 C U C
 C U A



1st position
degeneracy

if there is mutation in 1st or 3rd position
of codon → may cause some sense mutation



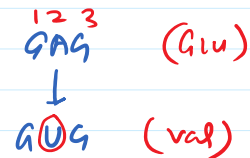
* Types of mutation in codon

① Same sense mutation / silent mutation

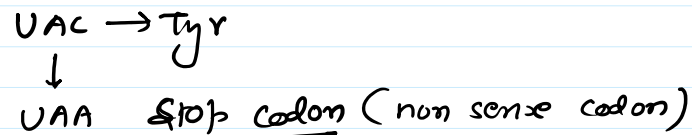
eg Proline, Leu.

② mis. sense mutation

eg- sickle cell anemia



③ Non-Sense mutation



• mutation in 2nd position
of codon is more harmful
than 3rd position

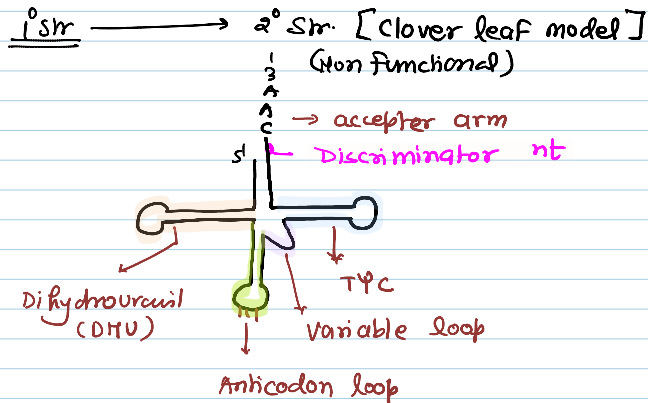
④ Single nt or double nt
insertion & deletion

↓
frame shift mutation.

Translation

- mRNA ✓
- ✓ → tRNA
- Ribosome

tRNA →



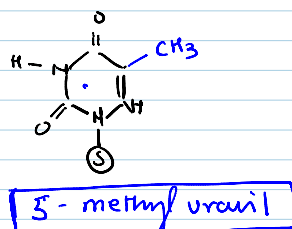
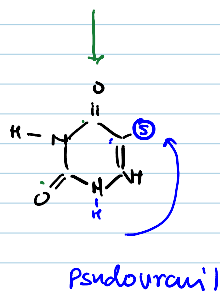
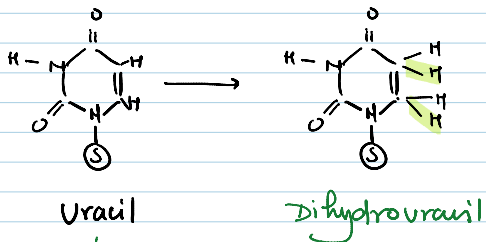
Post Transcriptional modification

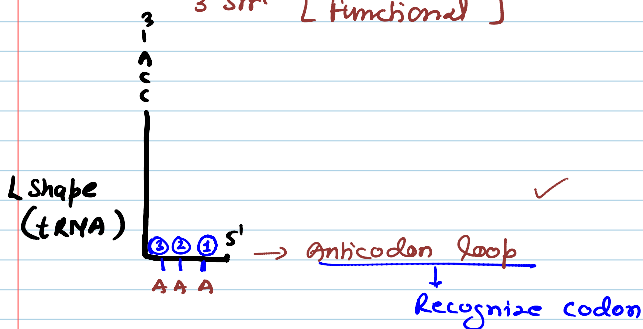
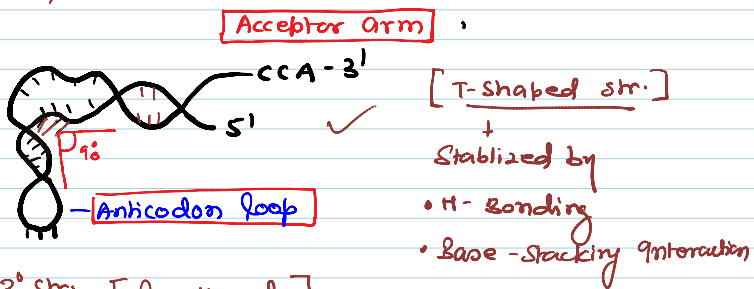
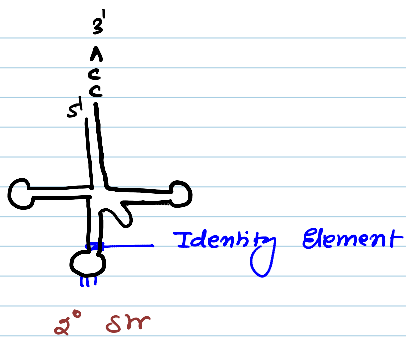
[A] → N⁷-methyl adenine

[G] → O⁶-methyl Guanine

[C] → 5-methyl Cytosine

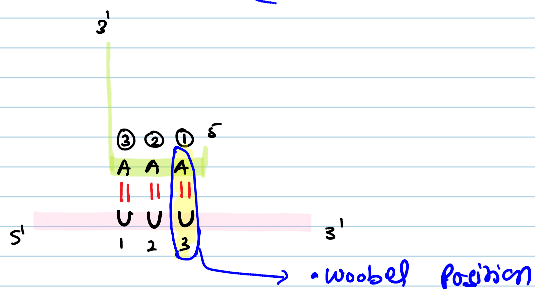
[U] → 5-methyl uracil
↳ Pseudouracil
↳ Dihydrouracil





#	Standard a.a	tRNA	Codon
	20	35	64

- tRNA can recognize more than one codon
- Reason → wobble position is 4th in 1st position of tRNA & 3rd position of codon (Anticodon)



- Flexibility is allowed
- Extended H-bonding can be

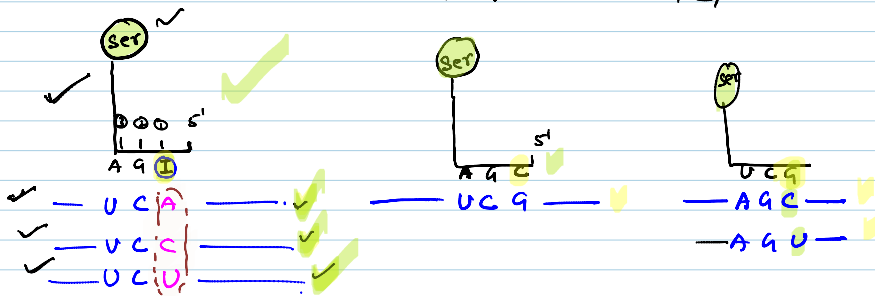
Seen

eq-

1 st position 5' Anticodon	3' codon-3 rd position
<p>A</p> <p>G</p> <p>C</p> <p>I (Inosine)</p>	<p>U</p> <p>C, U</p> <p>A</p> <p>A, C, U</p>

eq- Ser - has 6- codon

- more than 1 tRNA is needed



Iso acceptor tRNA

Different tRNA can accept same amino acid

Amino acid with 1 codon - one tRNA

a.a n 2 codon - 1 tRNA

a.a n 3 codon - 1 tRNA

a.a n 4 codon - 2 tRNA

& diff. tRNA that carry same a.a.

In mitochondria (Yeast & mammalian)

- only 20 tRNA + nt

→ more flexibility allowed than wobble flexibility

Plant mt → complete 35 tRNA present

loading of amino acid on tRNA -